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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Leadd B.V.
(B) STREET: Wassenaarseweg 72
(C) CITY: Leiden
(D) STATE: Zuid-Holland
(E) COUNTRY: the Netherlands
(F) POSTAL CODE (ZIP): 2333 AL

(A) NAME: Noteborn, Mathieu Hubertus Maria
(B) STREET: Sternstraat 15
(C) CITY: Leiderdorp
(D) STATE: Zuid-Holland
(E) COUNTRY: the Netherlands
(F) POSTAL CODE (ZIP): 2352 EH

(A) NAME: Damen-van Oorschot, Astrid Adriana Anna Maria
(B) STREET: Berliozplein 19
(C) CITY: Berkel en Rodenrijs
(D) STATE: Zuid-Holland
(E) COUNTRY: the Netherlands
(F) POSTAL CODE (ZIP): 2651 VG

(ii) TITLE OF INVENTION: Novel molecules involved in apoptotic pathways.

(iii) NUMBER OF SEQUENCES: 16

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/NL98/00687

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TACCACTACA ATGGATG

17

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Arg Asn Gly Gly Gly Glu Val Asp Arg Val Asp Tyr Asp Arg Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

Ins
EI

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Cys Gln Leu Arg Lys Glu Leu Gly Asp Ser Pro Lys Asp Lys Val Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 579..658
- (D) OTHER INFORMATION: /label= N
/note= "'N" stands for unknown."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGGGGATCAT GGAAGCTGAT AAAGATGACA CACAACAAAT TCTTAAGGAG
CATTCGCCAG 60

ATGAATTTAT AAAAGATGAA CAAAATAAGG GACTAATTGA TGAAATTACA
AAGAAAAATA 120

TTCAACTAAA GAAGGAGATC CAAAAGCTTG AAACGGAGTT ACAAGAGGCT
ACCAAAGAAT 180

TCCAGATTAA AGAGGATATT CCTGAAACAA AGATGAAATT CTTATCAGTT
GAAACTCCTG 240

AGAATGACAG CCAGTTGTCA AATATCTCCT GTTCGTTTCA AGTGAGCTCG
AAAGTTCCTT 300

ATGAGATACA AAAAGGACAA GCACTTATCA CCTTTGAAAA AGAAGAAGTT
GCTCAAAATG 360

TGGTAAGCAT GAGTAAACAT CATGTACAGA TAAAAGATGT AAATCTGGAG
GTTACGGCCA 420

AGCCAGTTCC ATTAAATTCA GGAGTCAGAT TCCAGGTTTA TGTAGAAGTT
TCTAAAATGA 480

AAATCAATGT TACTGAAATT CCTGACACAT TCGGTGAAGA TCAAATGAGA
GACAAACTAG 540

AGCTGAGCTT TTCAAAGTCC CGAAATGGGA GGCGGAGANG TGGACCGCGT
GGGACTATGA 600

CAGACAGTCC GGGAGTGCAG TCATCACGTT TGGNGGAGAT TGGGAGTGGC
TGACANNN 658

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 89..716
- (D) OTHER INFORMATION: /label= N
/note= ""N" stands for unknown."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGGAGTTACA AGAGGCTACC AAAGAATTCC AGATTAAAGA GGATATTCCT
GAAACAAAGA 60

TGAAATTCTT ATCAGTTGAA ACTCCTGANA ATGACAGCCA GTTGTCAAAT
ATCTCCTGTT 120

CGTTTCAAGG TGAGCTCGAA AGTTCCTTAT GAGATACAAA AAGGACAATG
CACTTATCAC 180

CTTTGAAAAA GGAAGAAAGTT GCTCAAAATG TGNGTAANGC ATGAGTAAAC
ATCATGTACA 240

GATAATAAGA TGTAATCTG GAGGTTACGG CCAAAGCCAA GTTCCATTAA
TATTCAAGGA 300

GTCANGATTC CAGNGTTTAT GCTAGAANGT TTCTAAAAAT GANAATCAAT
GGTTACTGGA 360

AATTCCTGGA CACATTGCGN TGAAAGATCA AGATGACGAA GACAAACTAA
GAAGCTGAGC 420

TTTTCAAAAG TCCCGAAANA TGGAAGAGCG GTAGAGGGTG GNACCGCGTG
NGANCTATGA 480

CAAGACAAGN CCGGGGAAGN TGCAGTCCAT CACGTTTGTN NGAAGATTGG
ANGTNGGCTG 540

ACCAANGAAT TTTGAAAAAG GAGANGAATT ACCCCTCTTT ANGAGTAANA
TCAAACCCT 600

GCCATAANAA GTTNACTGGT TTCNCCCATT ACACAGNANT TACANNTTGA
NCAANANTAN 660

NCAGGATAAT TTNCAGGGGA ANAATCTNAA GNATGGCAAG NTGACTTCTG
GACAANGGT 719

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

His Glu Gly Arg Gly Ile Met Glu Ala Asp Lys Asp Asp Thr Gln Gln
1 5 10 15

Ile Leu Lys Glu His Ser Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn
20 25 30

Lys Gly Leu Ile Asp Glu Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys
35 40 45

Glu Ile Gln Lys Leu Glu Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe
50 55 60

Gln Ile Lys Glu Asp Ile Pro Glu Thr Lys Met Lys Phe Leu Ser Val
65 70 75 80

Glu Thr Pro Glu Asn Asp Ser Gln Leu Ser Asn Ile Ser Cys Ser Phe
85 90 95

Gln Val Ser Ser Lys Val Pro Tyr Glu Ile Gln Lys Gly Gln Ala Leu
100 105 110

Ile Thr Phe Glu Lys Glu Glu Val Ala Gln Asn Val Val Ser Met Ser
115 120 125

Lys His His Val Gln Ile Lys Asp Val Asn Leu Glu Val Thr Ala Lys
130 135 140

Pro Val Pro Leu Asn Ser Gly Val Arg Phe Gln Val Tyr Val Glu Val
145 150 155 160

Ser Lys Met Lys Ile Asn Val Thr Glu Ile Pro Asp Thr Leu Arg Glu
165 170 175

Asp Gln Met Arg Asp Lys Leu Glu Leu Ser Phe Ser Lys Ser Arg Asn
180 185 190

Gly Arg Arg Arg Cys Gly Pro Arg Gly Thr Met Thr Asp Ser Pro Gly
195 200 205

Val Gln Ser Ser Arg Leu Val Glu Ile Gly Ser Gly
210 215 220

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Glu Ala Asp Lys Asp Asp Thr Gln Gln Ile Leu Lys Glu His Ser
1 5 10 15

Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn Lys Gly Leu Ile Asp Glu
20 25 30

Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys Glu Ile Gln Lys Leu Glu
35 40 45

Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe Gln Ile Lys Glu Asp Ile
50 55 60

Pro Glu Thr Lys Met Lys Phe Leu Ser Val Glu Thr Pro Glu Asn Asp
65 70 75 80

Ser Gln Leu Ser Asn Ile Ser Cys Ser Phe Gln Val Ser Ser Lys Val
85 90 95

Pro Tyr Glu Ile Gln Lys Gly Gln Ala Leu Ile Thr Phe Glu Lys Glu
100 105 110

Glu Val Ala Gln Asn Val Val Ser Met Ser Lys His His Val Gln Ile
115 120 125

Lys Asp Val Asn Leu Glu Val Thr Ala Lys Pro Val Pro Leu Asn Ser
130 135 140

Gly Val Arg Phe Gln Val Tyr Val Glu Val Ser Lys Met Lys Ile Asn

145	150	155	160
Val Thr Glu Ile Pro Asp Thr	Leu Arg Glu Asp Gln Met Arg Asp Lys		
165	170	175	
Leu Glu Leu Ser Phe Ser Lys Phe Arg Asn Gly Gly Gly Glu Val Asp			
180	185	190	
Arg Val Asp Tyr Asp Arg Gln Ser Gly Ser Ala Val Ile Thr Phe Val			
195	200	205	
Glu Ile Gly Val Ala Asp Lys Ile Leu Lys Lys Lys Glu Tyr Pro Leu			
210	215	220	
Tyr Ile Asn Gln Thr Cys His Arg Val Thr Val Ser Pro Tyr Thr Glu			
225	230	235	240
Ile His Leu Lys Lys Tyr Gln Ile Phe Ser Gly Thr Ser Lys Arg Thr			
245	250	255	
Val Leu Leu Thr Gly Met Glu Gly Ile Gln Met Asp Glu Glu Ile Val			
260	265	270	
Glu Asp Leu Ile Asn Ile His Phe Gln Arg Ala Lys Asn Gly Gly Gly			
275	280	285	
Glu Val Asp Val Val Lys Cys Ser Leu Gly Gln Pro His Ile Ala Tyr			
290	295	300	
Phe Glu Glu			
305			

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION:189..657

(D) OTHER INFORMATION:/label= N

/note= ""N" stands for unknown."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AGCAGGTGCT GCAACAAAAG GAGCACACGA TCAACATGGA GGAGTGCCGG
CTGCGGGTGC 60

AGGTCCAGCC CTTGGAGCTG CCCATGGTCA CCACCATCCA GGTGTCCAGC
CAGTTGAGTG 120

GCCGGAGGGT GTTGGTCACT GGATTTCCTG CCAGCCTCAG GCTGAGTGAG
GAGGAGCTGC 180

TGGACAANCT ANAGATCTTC TTTGGCAAGA CTAGGAACGG AGGTGGCNAT
GTGGACNTTC 240

GGGANCTACT GCCAGGGANT GTCATGCTGG GGTTTGCTAG GGATGGAGTG
GCTCANCCTC 300

TGTGCCAAAT CGGCCATTTC ACAGTGCCAC TGGGTGGGCA GCANGTCCCT
CTGAGAGTCT 360

CTCCGTATGT GAATGGGGAN ATCCAGANGG CTGANATCAG GTCNCAGCCA
NTTCCCCGCT 420

CGGTACTGGT GCTCAACATT CCTGATATCT TGGATGGCCC GGAGCTGCAT
GACGTCCTGG 480

ANATCCACTT CCAGAANCCC ACCCGCGGGG GCGGAGATGT AAGACGCCCT
GACAGTCGTA 540

CCCCAAGGAC AACAGGGCCT AACAGTCTTC ACCTCCTGAA TCAAGGCTAN
GGCCTCCCC 600

CTTCTCATCC TCCCCACCCC CCCCGCCAAA GGTTCCTCAAN ACTGGGCCTG
GGCTTTNTG 659

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 354..621
(D) OTHER INFORMATION: /label= N
/note= ""N" stands for unknown."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCAAAGTGGC TGAGCAGGTG CTGCAACAAA AGGAGCACAC GATCAACATG
GAGGAGTGCC 60

GGCTGCGGGT GCAGGTCCAG CCCTTGGAGC TGCCCATGGT CACCACCATC
CAGGTGTCCA 120

GCCAGTTGAG TGGCCGGAGG GTGTTGGTCA CTGGATTTC TGCCAGCCTC
AGGCTGAGTG 180

AGGAGGAGCT GCTGGACAAG CTAGAGATCT TCTTTGGCAA GACTAGGAAC
GGAGGTGGCG 240

ATGTGGACGT TCGGGAGCTA CTGCCAGGGA GTGTCATGCT GGGGTTTGCT
AGGGATGGAG 300

TGGCTCAGCG TCTGTGCCAA ATCGGCCAAG TTCACAGTGC CACTGGGTGG
GCANCAAGTC 360

CCTCTGAGAG TCTCTCCGTA TGTGAATGGG GAGATCCAGA AGGCTGAGAT
CAGGTCGCAN 420

CCAGTTCCCC NCTCGGTACT GGGTGCTCAA CATTCCTGAT ATCTTGGATT
GGCCCGGAGC 480

TGCATNACGT CCTGGANATC AACTTCANAA GCCCACCCGC CGGGGCNGNG
AGGTANAAGG 540

CCTGACATCN TTACCCCAA GGACAGCATG GNCCTAACAG TCCTCACCTC
CNAATCANGC 600

TNNGGGGCTN CCCTTCTANCNTCCCAACTG 630

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 182..626
- (D) OTHER INFORMATION: /label= N
/note= ""N" stands for unknown."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCACTG CCCTCTGCTT GCGGGCTCTG CTCTGATCAC CTTTGATGAC
CCCAAAGTGG 60

CTGAGCAGGT GCTGCAACAA AAGGAGCACA CGATCAACAT GGAGGAGTGC
CGGCTGCGGG 120

TGCAGGTCCA GCCCTTGGAG CTGCCCATGG TCACCACCAT CCAGGTGATG
GTGTCCAGCC 180

ANTTGAGTGG CCGGAGGGTG TTGGTCACTG GATTTCCTGC CAGCCTCAGG
CTGANTGAGG 240

AGGAGCTGCT GGACAAGCTA TGAGATCTTC TTTGGCAANA CTANGAACGG
ANGTGGCGAT 300

GTGGACGTTC GGGAGCTACT GCCAGGGAGT GTCATGCTGG GGTTCGCTAC
GGATGGAGTG 360

GCTCAGCGTC TGTGCCAAAT CGGCCAGTTC ACAAGTGCCA CTGGGTGGGC
AGCAAGTCCC 420

TCTGAGAGTC TCTCCGTATG TGANTGGNGA GATCAGAATG CTGANATTAA
GTCGCATCCA 480

ATTCCTCGCT CNGGTACTGG TGCTCANNAT CCTGANATCT TGGATTGGCC
CCNGANTNCA 540

TGANATCTGG NAGATTCAAT TNCANAAGTC CANCCNNCNG NGNCGGGAAG
TANANGCCCG 600

ANANTTCNTN NCNTANGGNC AGCANNGCCT G 631

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

His Glu Gly Pro Lys Val Ala Glu Gln Val Leu Gln Gln Lys Glu His
1 5 10 15

Thr Ile Asn Met Glu Glu Cys Arg Leu Arg Val Gln Val Gln Pro Leu
20 25 30

Glu Leu Pro Met Val Thr Thr Ile Gln Val Ser Ser Gln Leu Ser Gly
35 40 45

Arg Arg Val Leu Val Thr Gly Phe Pro Ala Ser Leu Arg Leu Ser Glu
50 55 60

Glu Glu Leu Leu Asp Lys Leu Glu Ile Phe Phe Gly Lys Thr Arg Asn
65 70 75 80

Gly Gly Gly Asp Val Asp Val Arg Glu Leu Leu Pro Gly Ser Val Met
 85 90 95
 Leu Gly Phe Ala Arg Asp Gly Val Ala Gln Arg Leu Cys Gln Ile Gly
 100 105 110
 Gln Val His Ser Ala Thr Gly Trp Ala Ser Ser Pro Ser Glu Ser Leu
 115 120 125
 Ser Val Cys Glu Trp Gly Asp Pro Glu Gly
 130 135

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ser Ala Pro Leu Asp Ala Ala Leu His Ala Leu Gln Glu Glu Gln
 1 5 10 15
 Ala Arg Leu Lys Met Arg Leu Trp Asp Leu Gln Gln Leu Arg Lys Glu
 20 25 30
 Leu Gly Asp Ser Pro Lys Asp Lys Val Pro Phe Ser Val Pro Lys Ile
 35 40 45
 Pro Leu Val Phe Arg Gly His Thr Gln Gln Asp Pro Glu Val Pro Lys
 50 55 60
 Ser Leu Val Ser Asn Leu Arg Ile His Cys Pro Leu Leu Ala Gly Ser
 65 70 75 80
 Ala Leu Ile Thr Phe Asp Asp Pro Lys Val Ala Glu Gln Val Leu Gln

85	90	95
Gln Lys Glu His Thr Ile Asn Met	Glu Glu Cys Arg Leu Arg Val Gln	
100	105	110
Val Gln Pro Leu Glu Leu Pro Met	Val Thr Thr Ile Gln Val Ser Ser	
115	120	125
Gln Leu Ser Gly Arg Arg Val Leu	Val Thr Gly Phe Pro Ala Ser Leu	
130	135	140
Arg Leu Ser Glu Glu Glu Leu Leu Asp	Lys Leu Glu Ile Phe Phe Gly	
145	150	155
Lys Thr Arg Asn Gly Gly Gly Asp	Val Asp Val Arg Glu Leu Leu Pro	
165	170	175
Gly Ser Val Met Leu Gly Phe Ala Arg	Asp Gly Val Ala Gln Arg Leu	
180	185	190
Cys Gln Ile Gly Gln Phe Thr Val	Pro Leu Gly Gly Gln Gln Val Pro	
195	200	205
Leu Arg Val Ser Pro Tyr Val Asn	Gly Glu Ile Gln Lys Ala Glu Ile	
210	215	220
Arg Ser Gln Pro Val Pro Arg Ser	Val Leu Val Leu Asn Ile Pro Asp	
225	230	235
Ile Leu Asp Gly Pro Glu Leu His	Asp Val Leu Glu Ile His Phe Gln	
245	250	255
Lys Pro Thr Arg Gly Gly Gly Gly	Arg Gly Pro Asp Ser Arg Thr Pro	
260	265	270
Arg Thr Ala Gly Pro Ser Ser Leu	His Leu	
275	280	

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

His Glu Gly Arg Ile His Cys Pro Leu Leu Ala Gly Ser Ala Leu Ile
1 5 10 15

Thr Phe Asp Asp Pro Lys Val Ala Glu Gln Val Leu Gln Gln Lys Glu
20 25 30

His Thr Ile Asn Met Glu Glu Cys Arg Leu Arg Val Gln Val Gln Pro
35 40 45

Leu Glu Leu Pro Met Val Thr Thr Ile Gln Val Met Val Ser Ser Xaa
50 55 60

Leu Ser Gly Arg Arg Val Leu Val Thr Gly Phe Pro Ala Ser Leu Arg
65 70 75 80

Leu Xaa Glu Glu Glu Leu Leu Asp Lys Leu Asp Leu Leu Trp Gln Xaa
85 90 95

Xaa Glu Arg Xaa Trp Arg Cys Gly Arg Ser Gly Ala Thr Ala Arg Glu
100 105 110

Cys His Ala Gly Val Cys Tyr Gly Trp Ser Gly Ser Ala Ser Val Pro
115 120 125

Asn Arg Pro Val His Lys Cys His Trp Val Gly Ser Lys Ser Leu Glu
130 135 140

Ser Leu Arg Met Xaa Xaa Arg Ser Glu Cys Xaa Val Ala Ser Asn Ser
145 150 155 160

Ser Leu Xaa Tyr Trp Cys Ser Xaa Ser Xaa Leu Gly Leu Ala Pro Xaa
165 170 175

Xaa Met Xaa Ser Gly Arg Phe Asn Xaa Xaa Ser Pro Xaa Xaa Xaa Xaa
180 185 190

Gly Lys Xaa Xaa Pro Xaa Xaa Ser Xaa Xaa Xaa Xaa Ser Xaa Ala
 195 200 205

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Arg Leu Arg Asn Gly His Val Gly Ile Ser Phe Val Pro Lys Glu Thr
 1 5 10 15

Gly Glu His Leu Val His Val Lys Lys Asn Gly Gln His Val Ala Ser
 20 25 30

Ser Pro Ile Pro Val Val Ile Ser Gln Ser Glu Ile Gly Asp Ala Ser
 35 40 45

Arg Val Arg Val Ser Gly Gln Gly Leu His Glu Gly His Thr Phe Glu
 50 55 60

Pro Ala Glu Phe Ile Ile Asp Thr Arg Asp Ala Gly Tyr Gly Gly Leu
 65 70 75 80

Ser Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn Thr Glu Asp
 85 90 95

Leu Glu Asp Gly Thr Cys Arg Val Thr Tyr Cys Pro Thr Glu Pro Gly
 100 105 110

Asn Tyr Ile Ile Asn Ile Lys Phe Ala Asp Gln His Val Pro Gly Ser
 115 120 125

Pro Phe Ser Val Lys Val Thr Gly Glu Gly Arg Val Lys Glu Ser Ile

130 135 140
Thr Arg Arg Arg Arg Ala Pro Ser Val Ala Asn Val Gly Ser His Cys
145 150 155 160
Asp Leu Ser Leu Lys Ile Pro Glu Ile Ser Ile Gln Asp Met Thr Ala
165 170 175
Gln Val Thr Ser Pro Ser Gly Lys Thr His Glu Ala Glu Ile Val Glu
180 185 190
Gly Glu Asn His Thr Tyr Cys Ile Arg Phe Val Pro Ala Glu Met Gly
195 200 205
Thr His Thr Val Ser Val Lys Tyr Lys Gly Gln His Val Pro Gly Ser
210 215 220
Pro Phe Gln Phe Thr Val Gly Pro Leu Gly Glu Gly Gly Ala His Lys
225 230 235 240
Val Arg Ala Gly Gly Pro Gly Leu Glu Arg Ala Glu Ala Gly Val Pro
245 250 255
Ala Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly Ala Gly Gly Leu Ala
260 265 270
Ile Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Ser Phe Glu Asp Arg
275 280 285
Lys Asp Gly Ser Cys Gly Val Ala Tyr Val Val Gln Glu Pro Gly Asp
290 295 300
Tyr Glu Val Ser Val Lys Phe Asn Glu Glu His Ile Pro Asp Ser Pro
305 310 315 320
Phe Val Val Pro Val Ala Ser Pro Ser Gly Asp Ala Arg Arg Leu Thr
325 330 335
Val Ser Ser Leu Gln Glu Ser Gly Leu Lys Val Asn Gln Pro Ala Ser
340 345 350
Phe Ala Val Ser Leu Asn Gly Ala Lys Gly Ala Ile Asp Ala Lys Val
355 360 365
His Ser Pro Ser Gly Ala Leu Glu Glu Cys Tyr Val Thr Glu Ile Asp

370 375 380
Gln Asp Lys Tyr Ala Val Arg Phe Ile Pro Arg Glu Asn Gly Val Tyr
385 390 395 400
Leu Ile Asp Val Lys Phe Asn Gly Thr His Ile Pro Gly Ser Pro Phe
405 410 415
Lys Ile Arg Val Gly Glu Pro Gly His Gly Gly Asp Pro Gly Leu Val
420 425 430
Ser Ala Tyr Gly Ala Gly Leu Glu Gly Gly Val Thr Gly Asn Pro Ala
435 440 445
Glu Phe Val Val Asn Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser Val
450 455 460
Thr Ile Asp Gly Pro Ser Lys Val Lys Met Asp Cys Gln Glu Cys Pro
465 470 475 480
Glu Gly Tyr Arg Val Thr Tyr Thr Pro Met Ala Pro Gly Ser Tyr Leu
485 490 495
Ile Ser Ile Lys Tyr Gly Gly Pro Tyr His Ile Gly Gly Ser Pro Phe
500 505 510
Lys Ala Lys Val Thr Gly Pro Arg Leu Val Ser Asn His Ser Leu His
515 520 525
Glu Thr Ser Ser Val Phe Val Asp Ser Leu Thr Lys Ala Thr Cys Ala
530 535 540
Pro Gln His Gly Ala Pro Gly Pro Gly Pro Ala Asp Ala Ser Lys Val
545 550 555 560
Val Ala Lys Gly Leu Gly Leu Ser Lys Ala Tyr Val Gly Gln Lys Ser
565 570 575
Ser Phe Thr Val Asp Cys Ser Lys Ala Gly Asn Asn Met Leu Leu Val
580 585 590
Gly Val His Gly Pro Arg Thr Pro Cys Glu Glu Ile Leu Val Lys His
595 600 605
Val Gly Ser Arg Leu Tyr Ser Val Ser Tyr Leu Leu Lys Asp Lys Gly

610 615 620
 Glu Tyr Thr Leu Val Val Lys Trp Gly His Glu His Ile Pro Gly Ser
 625 630 635 640
 Pro Tyr Arg Val Val Val Pro

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

His Glu Gly Arg Gly Val Thr Gly Asn Pro Ala Glu Phe Val Val Asn
 1 5 10 15
 Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser Val Thr Ile Asp Gly Pro
 20 25 30
 Ser Lys Val Lys Met Asp Cys Gln Glu Cys Pro Glu Gly Tyr Arg Val
 35 40 45
 Thr Tyr Thr Pro Met Ala Pro Gly Ser Tyr Leu Ile Ser Ile Lys Tyr
 50 55 60
 Gly Gly Pro Tyr His Ile Gly Gly Ser Pro Phe Lys Ala Lys Val Thr
 65 70 75 80
 Gly Pro Arg Leu Val Ser Asn His Ser Leu His Glu Thr Ser Ser Val
 85 90 95
 Phe Val Asp Ser Leu Thr Lys Ala Thr Cys Ala Pro His His Gly Ala
 100 105 110

Pro Gly Pro Gly Pro Ala Asp Ala Ser Lys Val Val Ala Lys Gly Leu
115 120 125

Gly Leu Ser Lys Ala Tyr Val Cys His Lys Ser Ser Phe Thr Val Asp
130 135 140

Cys Ser Lys Ala Cys Ile Ile Met Leu Leu Val Gly Val His Gly Pro
145 150 155 160

Trp Thr Pro Cys Asp Glu Ile Leu Val Lys Ala Arg Gly Gln Pro Ala
165 170 175

Leu Gln Arg Val Leu Thr Cys Phe Lys Asp Lys Gly Glu Val His Thr
180 185 190

Gly Gly Gln Asn Gly Gly Asp Tyr Gln Ile Pro Cys Lys Pro Leu Pro
195 200 205

Leu Cys Gly Cys Pro
210

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

His Glu Gly Arg Pro Thr Glu Pro Gly Asn Tyr Ile Ile Asn Ile Lys
1 5 10 15

Phe Ala Asp Gln His Val Pro Gly Ser Pro Phe Ser Val Lys Val Thr
20 25 30

Gly Glu Gly Arg Val Lys Glu Ser Ile Thr Arg Arg Arg Arg Ala Pro

35

40

45

Ser Val Ala Asn Val Gly Ser His Cys Asp Leu Ser Leu Lys Ile Pro

50

55

60

Glu Ile Ser Ile Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly

65

70

75

80

Lys Thr His Glu Ala Glu Ile Val Glu Gly Glu Asn His Thr Tyr Cys

85

90

95

Ile Arg Phe Val Pro Ala Glu Met Gly Thr His Thr Val Ser Val Lys

100

105

110

Tyr Lys Gly Gln His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly

115

120

125

Pro Leu Gly Glu Gly Gly Ala His Xaa Val Arg Ala Gly Gly Pro Gly

130

135

140

Leu Xaa Lys Ser Ser Trp Ser Ala Ser Arg Ile Gln Tyr Leu Gly Pro

145

150

155

160

Gly Lys Leu Val Leu Glu Ala Trp Pro Leu Leu Ser Xaa Ala Pro Ala

165

170

175

Xaa Leu Xaa Ser Leu Leu Arg Thr Ala Arg Thr Ala Pro Val Val Leu

180

185

190

Leu Met Leu Val Xaa Glu Pro Ser Asp Xaa Asn Pro Xaa Gln Val Ser

195

200

205

Thr Lys Glu His Xaa

210

Ins
E1